

O4CO
OIPERAW SEQUENCE LISTING
PATENT APPLICATION: US/09/652,292DATE: 09/21/2000
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3 <110> APPLICANT: Dawson, Paul
4   Bowden, Donald
5   Fossey, Sallyanne
7 <120> TITLE OF INVENTION: GLUT10: A NOVEL GLUCOSE TRANSPORTER IN THE TYPE 2 DIABETES LINKED REGION
8   OF CHROMOSOME 20Q12-13.1
10 <130> FILE REFERENCE: 9151.11
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,292
C--> 12 <141> CURRENT FILING DATE: 2000-08-31
12 <160> NUMBER OF SEQ ID NOS: 28
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 4395
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
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30 cagggcagga gggacagagg cgggggcggg ccggaaaagt tgccggcgcg cagcggcggt      180
32 ggggactccg gcgggggatg cgcgcccgcc ccctcagcgc cccacagcac ccgccgagtc      240
34 ccgctcgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg      291
35   Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val
36   1             5             10
38 tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca      339
39 Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
40 15             20             25             30
42 ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag      387
43 Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
44             35             40             45
46 cag gag ttc ctg gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc      435
47 Gln Glu Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser
48             50             55             60
50 ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc      483
51 Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
52             65             70             75
54 ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg      531
55 Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
56             80             85             90
58 gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc      579
59 Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
60 95             100             105             110
62 gcc att tcc ctc tcc atg gct tgc tgt atc tac gtg tca gag ctg      627
63 Ala Ile Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu
64             115             120             125
66 gtg ggg cca cgg cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc      675

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67 Val Gly Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly
68      130      135      140
70 atc acc gtg ggc atc ctg ctc tcc tat gcc ctc aac tat gca ctg gct      723
71 Ile Thr Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala
72      145      150      155
74 ggt acc ccc tgg gga tgg agg cac atg ttc ggc tgg gcc act gca cct      771
75 Gly Thr Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro
76      160      165      170
78 gct gtc ctg caa tcc ctc agc ctc ctc ttc ctc cct gct ggt aca gat      819
79 Ala Val Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp
80 175      180      185      190
82 gag act gca aca cac aag gac ctc atc cca ctc cag gga ggt gag gcc      867
83 Glu Thr Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala
84      195      200      205
86 ccc aag ctg ggc ccg ggg agg cca cgg tac tcc ttt ctg gac ctc ttc      915
87 Pro Lys Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe
88      210      215      220
90 agg gca cgc gat aac atg cga ggc cgg acc aca gtg ggc ctg ggg ctg      963
91 Arg Ala Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu
92      225      230      235
94 gtg ctc ttc cag caa cta aca ggg cag ccc aac gtg ctg tgc tat gcc      1011
95 Val Leu Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala
96      240      245      250
98 tcc acc atc ttc agc tcc gtt ggt ttc cat ggg gga tcc tca gcc gtg      1059
99 Ser Thr Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val
100 255      260      265      270
102 ctg gcc tct gtg ggg ctt ggc gca gtg aag gtg gca gct acc ctg acc      1107
103 Leu Ala Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr
104      275      280      285
106 gcc atg ggg ctg gtg gac cgt gca ggc cgc agg gct ctg ttg cta gct      1155
107 Ala Met Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala
108      290      295      300
110 ggc tgt gcc ctc atg gcc ctg tcc gtc agt ggc ata ggc ctc gtc agc      1203
111 Gly Cys Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser
112      305      310      315
114 ttt gcc gtg ccc atg gac tca ggc cca agc tgt ctg gct gtg ccc aat      1251
115 Phe Ala Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn
116      320      325      330
118 gcc acc ggg cag aca ggc ctc cct gga gac tct ggc ctg ctg cag gac      1299
119 Ala Thr Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp
120 335      340      345      350
122 tcc tct cta cct ccc att cca agg acc aat gag gac caa agg gag cca      1347
123 Ser Ser Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro
124      355      360      365
126 atc ttg tcc act gct aag aaa acc aag ccc cat ccc aga tct gga gac      1395
127 Ile Leu Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp
128      370      375      380
130 ccc tca gcc cct cct cgg ctg gcc ctg agc tct gcc ctc cct ggg ccc      1443
131 Pro Ser Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro

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132	385	390	395		
134 cct ctg ccc gct cgg ggg cat gca ctg ctg cgc tgg acc gca ctg ctg				1491	
135 Pro Leu Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu					
136 400	405	410			
138 tgc ctg atg gtc ttt gtc agt gcc ttc tcc ttt ggg ttt ggg cca gtg				1539	
139 Cys Leu Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val					
140 415	420	425	430		
142 acc tgg ctt gtc ctc agc gag atc tac cct gtg gag ata cga gga aga				1587	
143 Thr Trp Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg					
144 435	440	445			
146 gcc ttc gcc ttc tgc aac agc ttc aac tgg gcg gcc aac ctc ttc atc				1635	
147 Ala Phe Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile					
148 450	455	460			
150 agc ctc tcc ttc ctc gat ctc att ggc acc atc ggc ttg tcc tgg acc				1683	
151 Ser Leu Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr					
152 465	470	475			
154 ttc ctg ctc tac gga ctg acc gct gtc ctc ggc ctg ggc ttc atc tat				1731	
155 Phe Leu Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr					
156 480	485	490			
158 tta ttt gtt cct gaa aca aaa ggc cag tcg ttg gca gag ata gac cag				1779	
159 Leu Phe Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln					
160 495	500	505	510		
162 cag ttc cag aag aga cgg ttc acc ctg agc ttt ggc cac agg cag aac				1827	
163 Gln Phe Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn					
164 515	520	525			
166 tcc act ggc atc ccg tac agc cgc atc gag atc tct gcg gcc tcc tga				1875	
167 Ser Thr Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser					
168 530	535	540			
170 ggaatccgctc tgcctggaat tctggaactg tggttttggc agaccatctc cagcatcctg				1935	
172 ctctctaggc cccagagcac aagtccagc tggtcttttg ggagtggccc ctgcccccaa				1995	
174 aggtgggttg cttttgctgg ggtaaaaagg atgaaagtgt gagaatgccc aattcttcat				2055	
176 tttgggtttc aggccttgaa ggttcttgag gatctagtgt catgcctcgg tttccccatt				2115	
178 gacttggaca tttttgcagt ttttataaga agaataattct atgaagtctt tgttgcccca				2175	
180 tggatttttt tcaaagaatc tcaggggtac caatccgggc aggaggtttt tccccgatatc				2235	
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206 ataacaactc cctgaacctc agtttctca tctgcagaat ggggataatt atgtcccagg				3015	
208 ggtatattta gacctgttt cctttcagga ggggtccccc ctggtccagg gcctgggaaa				3075	
210 tttctactta tctctattac ccaggteccct cctttggacc ctgtaagggt tcagggtgaa				3135	

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216 tgtcatccat gcgtgcacat atgggtgctg gcagagcccc caaggactct ggctctcga 3315
218 gttctcctat cttctccatt ctatgctgtt cccttgatc cagtgaatg ctggagctgg 3375
220 ctttgccaag cttgtgagag ctggttgcta cattttcagg atttttaca gttggtaaac 3435
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224 aaaaaattat actcaaaatt cattacttaa ttttactacc tgttactatt atctgtgctt 3555
226 ttgaggctat ttctacatag taactcttat ggagacctag gggagacacc gcgcactctt 3615
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242 cagggatttt tattcgtagt ctaattttgt caaatcatgg ccaaatcgca gtgatagttg 4095
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246 ttggctatat ggaatttagg ataaagaata tttaacaata agaatattta caataaagag 4215
248 ttattatta ttgttaagtt gtgtgcaaca aacataccct ttatctctgt aaaatttata 4275
250 cacacaaaaa ttaacaaaag attctgtaag aattaattgg ctatatggaa tttaggatag 4335
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271 35 40 45
274 Phe Leu Val Gly Ser Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
275 50 55 60
278 Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
279 65 70 75 80
282 Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
283 85 90 95
286 Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
287 100 105 110
290 Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
291 115 120 125
294 Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
295 130 135 140
298 Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr
299 145 150 155 160
302 Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val
303 165 170 175
306 Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr

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315      210      215      220
318 Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
319 225      230      235      240
322 Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
323      245      250      255
326 Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
327      260      265      270
330 Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
331      275      280      285
334 Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Ala Gly Cys
335      290      295      300
338 Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala
339 305      310      315      320
342 Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
343      325      330      335
346 Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
347      340      345      350
350 Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
351      355      360      365
354 Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
355      370      375      380
358 Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
359 385      390      395      400
362 Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu
363      405      410      415
366 Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp
367      420      425      430
370 Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe
371      435      440      445
374 Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu
375      450      455      460
378 Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu
379 465      470      475      480
382 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
383      485      490      495
386 Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe
387      500      505      510
390 Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr
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395      530      535      540
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399 <211> LENGTH: 20
400 <212> TYPE: DNA
401 <213> ORGANISM: Artificial/Unknown

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date